



SEQUENCE LISTING

<110> Kahn, C. Ronald
Zhu, Jianhua

<120> MODULATING THE RAD-NM23 INTERACTION

<130> 10276-017002

<140> US 10/074,694
<141> 2002-02-12

<150> US 09/053,967
<151> 1998-04-02

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 308
<212> PRT
<213> Homo sapiens

<400> 1
Met Thr Leu Asn Gly Gly Gly Ser Gly Ala Gly Gly Ser Arg Gly Gly
1 5 10 15
Gly Gln Glu Arg Glu Arg Arg Arg Gly Ser Thr Pro Trp Gly Pro Ala
20 25 30
Pro Pro Leu His Arg Arg Ser Met Pro Val Asp Glu Arg Asp Leu Gln
35 40 45
Ala Ala Leu Thr Pro Gly Ala Leu Thr Ala Ala Ala Ala Gly Thr Gly
50 55 60
Thr Gln Gly Pro Arg Leu Asp Trp Pro Glu Asp Ser Glu Asp Ser Leu
65 70 75 80
Ser Ser Gly Gly Ser Asp Ser Asp Glu Ser Val Tyr Lys Val Leu Leu
85 90 95
Leu Gly Ala Pro Gly Val Gly Lys Ser Ala Leu Ala Arg Ile Phe Gly
100 105 110
Gly Val Glu Asp Gly Pro Glu Ala Glu Ala Ala Gly His Thr Tyr Asp
115 120 125
Arg Ser Ile Val Val Asp Gly Glu Glu Ala Ser Leu Met Val Tyr Asp
130 135 140
Ile Trp Glu Gln Asp Gly Gly Arg Trp Leu Pro Gly His Cys Met Ala
145 150 155 160
Met Gly Asp Ala Tyr Val Ile Val Tyr Ser Val Thr Asp Lys Gly Ser
165 170 175
Phe Glu Lys Ala Ser Glu Leu Arg Val Gln Leu Arg Arg Ala Arg Gln
180 185 190
Thr Asp Asp Val Pro Ile Ile Leu Val Gly Asn Lys Ser Asp Leu Val
195 200 205
Arg Ser Arg Glu Val Ser Val Asp Glu Gly Arg Ala Cys Ala Val Val
210 215 220
Phe Asp Cys Lys Phe Ile Glu Thr Ser Ala Ala Leu His His Asn Val
225 230 235 240

Gln Ala Leu Phe Glu Gly Val Val Arg Gln Ile Arg Leu Arg Arg Asp
 245 250 255
 Ser Lys Glu Ala Asn Ala Arg Arg Gln Ala Gly Thr Arg Arg Arg Glu
 260 265 270
 Ser Leu Gly Lys Lys Ala Lys Arg Phe Leu Gly Arg Ile Val Ala Arg
 275 280 285
 Asn Ser Arg Lys Met Ala Phe Arg Ala Lys Ser Lys Ser Cys His Asp
 290 295 300
 Leu Ser Val Leu
 305

<210> 2
 <211> 664
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)...(498)

<400> 2
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 Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
 1 5 10 15

aac agt gag cgt acc ttc att gcc atc aag cct gat ggg gtc cag cg 96
 Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
 20 25 30

ggg ctg gtg ggc gag atc atc aag cgg ttc gag cag aag ggg ttc cgc 144
 Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
 35 40 45

ctt gtt ggt ctg aag ttt ctg cag gct tca gag gac ctt ctc aag gag 192
 Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
 50 55 60

cac tac act gac ctg aag gac cgc ccc ttc ttt act ggc ctg gtg aaa 240
 His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
 65 70 75 80

tac atg cac tca gga cca gtg gtt gct atg gtc tgg gag ggt ctg aat 288
 Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
 85 90 95

gtg gtg aag aca ggc cgc gtg atg ctt gga gag acc aac ccc gca gac 336
 Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
 100 105 110

tct aag cct ggg acc ata cga gga gac ttc tgc att caa gtt ggc agg 384
 Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
 115 120 125

aac atc att cat ggc agc gat tct gta aag agc gca gag aag gag atc 432
 Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
 130 135 140

agc ttg tgg ttt cag cct gag gag ctg gtg gag tac aag agc tgt gcg 480
 Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
 145 150 155 160

cag aac tgg atc tat gag tgataggacg gtgccggttt tctaccgtct 528
 Gln Asn Trp Ile Tyr Glu
 165

tactcttggtt ctcacaggca ggggaccagc aacccttagat atttctggaa cttctttgac 588
 ctggaaggaa cctttggag ccgtgactcc ctgtgcagtg ttacgtgccca ctgttagatt 648
 aaagtgttta atctgt 664

<210> 3
<211> 166
<212> PRT
<213> Mus musculus

<400> 3
Gln Ser Gln Pro Ala Val Lys Pro Cys His Leu Lys Gly Thr Met Ala
 1 5 10 15
Asn Ser Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg
 20 25 30
Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg
 35 40 45
Leu Val Gly Leu Lys Phe Leu Gln Ala Ser Glu Asp Leu Leu Lys Glu
 50 55 60
His Tyr Thr Asp Leu Lys Asp Arg Pro Phe Phe Thr Gly Leu Val Lys
 65 70 75 80
Tyr Met His Ser Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn
 85 90 95
Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp
 100 105 110
Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg
 115 120 125
Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys Glu Ile
 130 135 140
Ser Leu Trp Phe Gln Pro Glu Glu Leu Val Glu Tyr Lys Ser Cys Ala
 145 150 155 160
Gln Asn Trp Ile Tyr Glu
 165

<210> 4
<211> 670
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (73) ... (528)

<400> 4
cggccacgag gcggaatccc ttctgctctc ccagcgacgc gccggccccc ggccccctcca 60
gcttcccgga cc atg gcc aac ctg gag cgc acc ttc atc gcc atc aag ccg 111
Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro
 1 5 10

gac ggc gtg cag cgc ggc ctg gtg ggc gag atc atc aag cgc ttc gag	159
Asp Gly Val Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu	
15 20 25	
cag aag gga ttc cgc ctc gtg gcc atg aag ttc ctc cg ^g gcc tct gaa	207
Gln Lys Gly Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu	
30 35 40 45	
gaa cac ctg aag cag cac tac att gac ctg aaa gac cga cca ttc ttc	255
Glu His Leu Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe	
50 55 60	
cct ggg ctg gtg aag tac atg aac tca ggg ccg gtt gtg gcc atg gtc	303
Pro Gly Leu Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val	
65 70 75	
tgg gag ggg ctg aac gtg gtg aag aca ggc cga gtg atg ctt ggg gag	351
Trp Glu Gly Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu	
80 85 90	
acc aat cca gca gat tca aag cca ggc acc att cgt ggg gac ttc tgc	399
Thr Asn Pro Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys	
95 100 105	
att cag gtt ggc agg aac atc att cat ggc agt gat tca gta aaa agt	447
Ile Gln Val Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser	
110 115 120 125	
gct gaa aaa gaa atc agc cta tgg ttt aag cct gaa gaa ctg gtt gac	495
Ala Glu Lys Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp	
130 135 140	
tac aag tct tgt gct cat gac tgg gtc tat gaa taagaggtgg acacaacagc 548	
Tyr Lys Ser Cys Ala His Asp Trp Val Tyr Glu	
145 150	
agtctccttc agcacggcgt ggtgtgtccc tggacacagc tcttcattcc attgacttag 608	
aggcaacagg attgatcatt ctttataga gcataattgc caataaagct tttggaagcc 668	
gg 670	
<210> 5	
<211> 152	
<212> PRT	
<213> Homo sapiens	
<400> 5	
Met Ala Asn Leu Glu Arg Thr Phe Ile Ala Ile Lys Pro Asp Gly Val	
1 5 10 15	
Gln Arg Gly Leu Val Gly Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly	
20 25 30	
Phe Arg Leu Val Ala Met Lys Phe Leu Arg Ala Ser Glu Glu His Leu	
35 40 45	
Lys Gln His Tyr Ile Asp Leu Lys Asp Arg Pro Phe Phe Pro Gly Leu	
50 55 60	
Val Lys Tyr Met Asn Ser Gly Pro Val Val Ala Met Val Trp Glu Gly	
65 70 75 80	

Leu Asn Val Val Lys Thr Gly Arg Val Met Leu Gly Glu Thr Asn Pro
85. 90 95
Ala Asp Ser Lys Pro Gly Thr Ile Arg Gly Asp Phe Cys Ile Gln Val
100 105 110
Gly Arg Asn Ile Ile His Gly Ser Asp Ser Val Lys Ser Ala Glu Lys
115 120 125
Glu Ile Ser Leu Trp Phe Lys Pro Glu Glu Leu Val Asp Tyr Lys Ser
130 135 140
Cys Ala His Asp Trp Val Tyr Glu
145 150